

# SEQUENCE LISTING

<110> Cahoon, Edgar B.  
Cahoon, Rebecca E.  
Kinney, Anthony J.  
Rafalski, J. Antoni

<120> TRIACYLGLYCEROL LIPASES

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<151> 1988-04-30

<150> PCT/US99/09280

<151> 1999-04-29

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<213> Zea mays

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<213> Zea mays

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His Phe Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr
    35                               40                               45
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Val Leu Pro Glu Arg Asn Ile Ala Ser Tyr Gly Gln Ala Glu Pro Pro
    50                               55                               60
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Val Tyr Arg Met Ser Gly Ile Pro Pro Ser Phe Pro Leu Phe Leu Ser  
65 70 75 80

Tyr Gly Gly Arg Asp Ser Leu Ala Asp Pro Ala Asp Val Arg Leu Leu  
85 90 95

Leu Gln Asp Leu Arg Gly His Asp Gln Asp Lys Leu Thr Val Gln Tyr  
100 105 110

Leu Asp Lys Phe Ala His Leu Asp Phe Ile Ile Gly Val Cys Ala Lys  
115 120 125

Asp Tyr Val Tyr Lys Asp Met Ile Asp Phe Leu Asn Arg Phe Asn  
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<213> Catalpa sp.

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35 40 45

Pro Leu Phe Leu Ser Tyr Gly Gly Gln Asp Ala Leu Ser Asp Val Lys  
50 55 60

Asp Val Glu Thr Leu Leu Asp Ser Leu Lys Leu His Asp Val Asp Lys  
65 70 75 80

Leu His Val Gln Tyr Ile Lys Asp Tyr Ala His Ala Asp Phe Ile Ile  
85 90 95

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Arg Asn Gln Ala  
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Phe Leu Pro Gln Asn Asp Val Val Leu Pro Pro Asp Gly Val Cys Ser  
35 40 45



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Lys Ala Asn Asn Gly Gly His Gly Ala Pro Arg Lys Ser Ala Cys Xaa  
1 5 10 15

Ala Pro Ala Pro Pro Pro Arg Val Pro Leu Pro Pro Ser Arg Trp Ser  
20 25 30

Pro Arg Ile Pro Ala His Arg Arg Ala Thr Pro Arg Leu Pro Ala Arg  
35 40 45

Gly Gly Arg Trp Pro Leu Pro Ala Ala Ala Pro Ala Ala Gly Tyr Pro  
50 55 60

Cys Thr Glu His Thr Val Gln Thr Asp Asp Gly Phe Leu Leu Ser Leu  
65 70 75 80

Gln His Ile Pro His Gly Arg Asn Gly Ile Ala Asp Asn Thr Gly Pro  
85 90 95

Pro Val Phe Leu Gln His Gly Leu Phe Gln Gly Gly Asp Thr Trp Phe  
100 105 110

Ile Asn Ser Asn Glu Gln Ser Leu Gly Tyr Ile Leu Ala Asp Asn Gly  
115 120 125

Phe Asp Val Trp Val Gly Asn Val Arg Gly Thr Arg Trp Ser Lys Gly  
130 135 140

His Ser Thr Leu Ser Val His Asp Lys Leu Phe Trp Asp Trp Ser Trp  
145 150 155 160

Gln Asp Leu Ala Glu Tyr Asp Val Leu Ala Met Leu Ser Tyr Val Tyr  
165 170 175

Thr Val Ala Gln Ser Lys Ile Leu Tyr Val Gly His Ser Gln Gly Thr  
180 185 190

Ile Met Gly Leu Ala Ala Phe Thr Met Pro Glu Thr Val Lys Met Ile  
195 200 205

Ser Ser Ala Ala Leu Leu Cys Pro Ile Ser Tyr Leu Asp His Val Ser  
210 215 220

Ala Ser Phe Val Leu Arg Ala Val Ala Met His Leu Asp Glu Met Leu  
225 230 235 240

Val Ile Met Gly Ile His Gln Leu Asn Phe Arg Ser Asp Met Gly Val  
245 250 255

Gln Ile Leu Asp Ser Leu Cys Asp Asp Glu His Leu Asp Cys Asn Asp  
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<213> Zea mays

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Arg Asn Thr Thr Asn Asp Ile Ser Asp Asp Lys Cys Pro Pro Gln Pro  
35 40 45  
His Pro Leu Xaa Met Cys Arg Ser Arg Val Ala Ala Tyr Gly Tyr Pro  
50 55 60  
Cys Glu Glu Tyr His Val Thr Thr Glu Asp Gly Tyr Ile Leu Ser Leu  
65 70 75 80  
Lys Lys Ile Pro Tyr Gly Leu Ser Gly Xaa Thr Xaa Ile Thr Arg Xaa  
85 90 95  
Pro Val Leu Leu Phe His Gly Leu Leu Val Asp Gly Phe Cys Trp Val  
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<213> Zea mays

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      20          25          30

Gln Thr Gly Gln Lys Pro His Tyr Val Gly His Ser Met Gly Thr Leu
      35          40          45

Val Ala Leu Ala Ala Phe Ser Glu Gly Arg Val Val Ser Gln Leu Lys
      50          55          60

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Ser Ala Ala Leu Leu Thr Pro Val Ala Tyr Leu Xaa His Xaa Asn Xaa  
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<212> DNA  
<213> Oryza sativa

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<212> PRT  
<213> Oryza sativa

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20 25 30  
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35 40 45  
Gln Leu Leu Leu Pro Leu Gly Tyr Pro Cys Thr Glu His Asn Val Glu  
50 55 60  
Thr Lys Asp Gly Phe Leu Leu Ser Leu Gln His Ile Pro His Gly Lys  
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20 25 30  
His Leu Ala Gln Thr Val Arg Asp Gly Val Leu Thr Lys Tyr Asp Tyr  
35 40 45  
Val Met Pro Asp Ala Asn Val Ala Arg Tyr Gly Gln Xaa Asp Pro Pro  
50 55 60  
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<212> DNA  
<213> Glycine max

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<211> 410  
<212> PRT  
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<400> 18  
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Leu Gly Arg Asn Ile Asn Pro Ser Val Tyr Gly Ile Cys Ala Ser Ser  
35 40 45  
Val Ile Val His Gly Tyr Lys Cys Gln Glu His Glu Val Thr Thr Asp  
50 55 60  
Asp Gly Tyr Ile Leu Ser Leu Gln Arg Ile Pro Glu Gly Arg Gly Lys  
65 70 75 80  
Ser Ser Gly Ser Gly Thr Arg Lys Gln Pro Val Val Ile Gln His Gly  
85 90 95  
Val Leu Val Asp Gly Met Thr Trp Leu Leu Asn Pro Pro Glu Gln Asp  
100 105 110

Leu	Pro	Leu	Ile	Leu	Ala	Asp	Asn	Gly	Phe	Asp	Val	Trp	Ile	Ala	Asn
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	130					135					140				
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Phe	Pro	Ala	Val	Phe	Asn	Tyr	Val	Phe	Ser	Gln	Thr	Gly	Gln	Lys	Ile
				165					170					175	
Asn	Tyr	Val	Gly	His	Ser	Leu	Gly	Thr	Leu	Val	Ala	Leu	Ala	Ser	Phe
			180					185					190		
Ser	Glu	Gly	Lys	Leu	Val	Thr	Gln	Leu	Lys	Ser	Ala	Ala	Leu	Leu	Ser
		195					200					205			
Pro	Ile	Ala	Tyr	Leu	Ser	His	Met	Asn	Thr	Ala	Leu	Gly	Val	Val	Ala
	210					215					220				
Pro	Lys	Ser	Phe	Val	Gly	Glu	Ile	Thr	Thr	Leu	Phe	Gly	Leu	Ala	Glu
225					230					235					240
Phe	Asn	Pro	Lys	Gly	Leu	Ala	Val	Asp	Ala	Phe	Leu	Lys	Ser	Leu	Cys
				245					250					255	
Ala	His	Pro	Gly	Ile	Asp	Cys	Tyr	Asp	Leu	Leu	Thr	Ala	Leu	Thr	Gly
			260					265					270		
Lys	Asn	Cys	Cys	Leu	Asn	Ser	Ser	Thr	Val	Asp	Leu	Phe	Leu	Met	Asn
		275					280					285			
Glu	Pro	Gln	Ser	Thr	Ser	Thr	Lys	Asn	Met	Val	His	Leu	Ala	Gln	Thr
	290					295					300				
Val	Arg	Leu	Gly	Ala	Leu	Thr	Lys	Phe	Asn	Tyr	Val	Arg	Pro	Asp	Tyr
305					310					315					320
Asn	Ile	Met	His	Tyr	Gly	Glu	Ile	Phe	Pro	Pro	Ile	Tyr	Asn	Leu	Ser
				325					330					335	
Asn	Ile	Pro	His	Asp	Leu	Pro	Leu	Phe	Ile	Ser	Tyr	Gly	Gly	Arg	Asp
			340					345					350		
Ala	Leu	Ser	Asp	Val	Arg	Asp	Val	Glu	Asn	Leu	Leu	Asp	Lys	Leu	Lys
		355					360					365			
Phe	His	Asp	Glu	Asn	Lys	Arg	Ser	Val	Gln	Phe	Ile	Gln	Glu	Tyr	Ala
	370					375					380				
His	Ala	Asp	Tyr	Ile	Met	Gly	Phe	Asn	Ala	Lys	Asp	Leu	Val	Tyr	Asn
385					390					395					400
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				405					410						

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<210> 19
<211> 1438
<212> DNA
<213> Glycine max
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 Ile Asn Tyr Ile Asn Ser Val Thr Asn Ser Lys Ile Phe Val Val Gly  
 165 170 175  
 His Ser Gln Gly Thr Ile Ile Ser Leu Ala Ala Phe Thr Gln Pro Glu  
 180 185 190  
 Ile Val Glu Lys Val Glu Ala Ala Ala Leu Leu Ser Pro Ile Ser Tyr  
 195 200 205  
 Leu Asp His Val Ser Ala Pro Leu Val Leu Arg Met Val Lys Met His  
 210 215 220  
 Ile Asp Glu Met Ile Leu Thr Met Gly Ile His Gln Leu Asn Phe Lys  
 225 230 235 240  
 Ser Glu Trp Gly Ala Ser Leu Leu Val Ser Leu Cys Asp Thr Arg Leu  
 245 250 255  
 Ser Cys Asn Asp Met Leu Ser Ser Ile Thr Gly Lys Asn Cys Cys Phe  
 260 265 270  
 Asn Glu Ser Arg Val Glu Phe Tyr Leu Glu Gln Glu Pro His Pro Ser  
 275 280 285  
 Ser Ser Lys Asn Leu Asn His Leu Phe Gln Met Ile Arg Lys Gly Thr  
 290 295 300  
 Tyr Ser Lys Tyr Asp Tyr Gly Lys Leu Lys Asn Leu Ile Glu Tyr Gly  
 305 310 315 320  
 Lys Phe Asn Pro Pro Lys Phe Asp Leu Ser Arg Ile Pro Lys Ser Leu  
 325 330 335  
 Pro Leu Trp Met Ala Tyr Gly Gly Asn Asp Ala Leu Ala Asp Ile Thr  
 340 345 350  
 Asp Phe Gln His Thr Leu Lys Glu Leu Pro Ser Pro Pro Glu Val Val  
 355 360 365  
 Tyr Leu Glu Asn Tyr Gly His Val Asp Phe Ile Leu Ser Leu Gln Ala  
 370 375 380  
 Lys Gln Asp Leu Tyr Asp Pro Met Ile Ser Phe Phe Lys Ser Ser Gly  
 385 390 395 400  
 Lys Phe Ser Ser Met  
 405

<210> 21  
 <211> 737  
 <212> DNA  
 <213> Zea mays

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 tcccaagaac aatccgtgtg acccatcaga atgatattgt gccgcattta ccaccgtatt 180  
 attattacct aggtgaatgg acataccacc acttcgctag agaggtttgg cttcatgaga 240



gcatagatgg aaatgtagtt accagaaaacg agacgggtatg tgatgattct ggtgaagacc 300  
cgacctgtag caggtcggtc tatgggatga gcgtagcaga tcatcttgag tactatgatg 360  
tcacactaca tgctgattca agaggaacct gtcaattcgt gattggtgca gccaaccaag 420  
tatacaacta cgttcgtgaa gttgatggat ccatcatcct gtcaagatac ccgcaagaac 480  
cacaagctct agaatctatg tgactttgta tgccacggaa tgcacccctg tacagtattt 540  
ttcattttca ttttgtgtac agctcatgaa atgctgggcg ctcttgagc tctccagagg 600  
ataaggagag gctcaccttt ttaaattgtgc cccctttgct caagtgagaa tcgtgcatgt 660  
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taaaaaaaaa aaaaaaa 737

<210> 22  
<211> 166  
<212> PRT  
<213> Zea mays

<400> 22  
Thr Arg Phe Cys Ala Leu Asp Leu Ser Val Lys Phe Gly Ser Gln Glu  
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Val Glu Leu Met Thr Phe Gly Gln Pro Arg Ile Gly Asn Pro Ala Phe  
20 25 30  
Ala Val Tyr Phe Gly Glu Gln Val Pro Arg Thr Ile Arg Val Thr His  
35 40 45  
Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Tyr Tyr Tyr Leu Gly  
50 55 60  
Glu Trp Thr Tyr His His Phe Ala Arg Glu Val Trp Leu His Glu Ser  
65 70 75 80  
Ile Asp Gly Asn Val Val Thr Arg Asn Glu Thr Val Cys Asp Asp Ser  
85 90 95  
Gly Glu Asp Pro Thr Cys Ser Arg Ser Val Tyr Gly Met Ser Val Ala  
100 105 110  
Asp His Leu Glu Tyr Tyr Asp Val Thr Leu His Ala Asp Ser Arg Gly  
115 120 125  
Thr Cys Gln Phe Val Ile Gly Ala Ala Asn Gln Val Tyr Asn Tyr Val  
130 135 140  
Arg Glu Val Asp Gly Ser Ile Ile Leu Ser Arg Tyr Pro Gln Glu Pro  
145 150 155 160  
Gln Ala Leu Glu Ser Met  
165

<210> 23  
<211> 1434  
<212> DNA  
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20 25 30

Ala Xaa Ala Val Tyr Met Thr Asp Leu Thr Ala Leu Phe Thr Trp Thr  
50 55 60

Ile Val Asp Val Glu Lys Leu Leu Ala Gly Ile Val Gly Val Asp His  
85 90 95

Val Gln Asn Trp Ile Lys Asp Leu Ile Trp Lys Gln Leu Asp Leu Ser  
115 120 125

Tyr Asn Asn Thr Ile Leu Arg Leu Ala Ile Thr Ser Ala Val His Lys  
145 150 155 160

Met Gly Gly Ala Met Ala Ser Phe Cys Ala Leu Asp Leu Ala Met Lys  
180 185 190

Gly Asn Ala Ala Phe Ala Ser Tyr Phe Ala Lys Tyr Val Pro Asn Thr  
210 215 220

Phe Ser Phe Leu Pro Gln Leu Thr Tyr His His Phe Pro Arg Glu Val  
245 250 255

Ser Gly Glu Asp Pro Asp Cys Cys Arg Cys Ile Ser Met Phe Gly Leu  
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 <211> 1560  
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 <213> Zea mays

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 <221> unsure  
 <222> (601)

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 gcgtctccgc cgccgcggga tccggcgga tgactactac ttggacgtgg agagcggcag 180  
 gcggcggtgc cgctggtgca gcagcagtag gtgaacgggc ggctcgtccg cctccgcacc 240  
 ttctccgtgt tcgaggtgag catgatggcc gccaaagatcg cctacgagaa cgccgcctac 300  
 atcgagaacg tcgtcaacaa cgtctggaag ttccacttcg tggggttcta caactgctgg 360  
 aacaagtctg tgggcgacca cagcagcgag gcgttcgtgt tcaccgacaa ggcaagagga 420  
 cgcgagcgtg gtggtggtgt cgttcggggg cagcgagccc ttcaacatgc gggactggtc 480  
 cagcgacgta aacctgtcgt ggctgggcat gggcgagctg ggccacgtcc acgtcggctt 540  
 cctcaaggcg ctgggcctgc aggaggagga gccacgcggg cgttccccaa 600  
 nggcgcccc aacgccgtcc cgggcaagcc gctggcctac tacgcgctgc gcgaggaggt 660  
 ccagaagcag ctgcagaagc acccgaacgc caacgctcgt gtcaccggcc acagcctcgg 720  
 cgccgcgctg gcgacctct tcccggcgt gctggcgctt cacggggagc ggggcgtcct 780  
 ggaccgcctg ctctccgtgg tcacctacgg gcagccgcgc gtgggcgaca aggtgttcgc 840  
 gggctacgtg cgcgccaacg tgcccgtgga gccgctccgg gtggtgtacc gctacgacgt 900  
 ggtcccgcgc gtgcccttcg acgcgcgcgc cgtcgcgcac ttgcgcgcac gcggcacctg 960  
 cgtctacttc gacggctggt acaagggccg cgagatcgcc aagggcggcg acgcgccc aa 1020  
 caagaactac ttcgaccca ggtacctgct gtccatgtac ggcaacgcgt ggggggacct 1080  
 cttcaaggcg gccttcctgt gggccaagga gggcaaggac taccgcgagg gcgcgctctc 1140  
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 ctacgtcaac gccgtccgcc tcggcagcgt cgctcggcg tagcttttgg attgcatgtt 1260  
 cgtttccatg catgtgtatc attgcatgca ataattggat gaaataaaca gcaataagct 1320  
 tcatcagtat tattattgtt gttgttgaat atatgcatcc tctcctctct atatagaatt 1380  
 atagatacat gaggcctggc cggccgcgca cgttgtgtgaa cagttgaagc gcttcccaaa 1440  
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<210> 26  
 <211> 258  
 <212> PRT  
 <213> Zea mays

<220>  
 <221> UNSURE  
 <222> (45)

<400> 26  
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 Glu Leu Gly His Val His Val Gly Phe Leu Lys Ala Leu Gly Leu Gln  
 20 25 30  
 Glu Glu Asp Gly Lys Asp Ala Thr Arg Ala Phe Pro Xaa Gly Ala Pro  
 35 40 45  
 Asn Ala Val Pro Gly Lys Pro Leu Ala Tyr Tyr Ala Leu Arg Glu Glu  
 50 55 60

Val Gln Lys Gln Leu Gln Lys His Pro Asn Ala Asn Val Val Val Thr  
 65 70 75 80  
 Gly His Ser Leu Gly Ala Ala Leu Ala Thr Ile Phe Pro Ala Leu Leu  
 85 90 95  
 Ala Phe His Gly Glu Arg Gly Val Leu Asp Arg Leu Leu Ser Val Val  
 100 105 110  
 Thr Tyr Gly Gln Pro Arg Val Gly Asp Lys Val Phe Ala Gly Tyr Val  
 115 120 125  
 Arg Ala Asn Val Pro Val Glu Pro Leu Arg Val Val Tyr Arg Tyr Asp  
 130 135 140  
 Val Val Pro Arg Val Pro Phe Asp Ala Pro Pro Val Ala Asp Phe Ala  
 145 150 155 160  
 His Gly Gly Thr Cys Val Tyr Phe Asp Gly Trp Tyr Lys Gly Arg Glu  
 165 170 175  
 Ile Ala Lys Gly Gly Asp Ala Pro Asn Lys Asn Tyr Phe Asp Pro Arg  
 180 185 190  
 Tyr Leu Leu Ser Met Tyr Gly Asn Ala Trp Gly Asp Leu Phe Lys Gly  
 195 200 205  
 Ala Phe Leu Trp Ala Lys Glu Gly Lys Asp Tyr Arg Glu Gly Ala Val  
 210 215 220  
 Ser Leu Leu Tyr Arg Ala Thr Gly Leu Leu Val Pro Gly Ile Ala Ser  
 225 230 235 240  
 His Ser Pro Arg Asp Tyr Val Asn Ala Val Arg Leu Gly Ser Val Ala  
 245 250 255

Ser Ala

<210> 27  
 <211> 432  
 <212> DNA  
 <213> Oryza sativa

<220>  
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 <222> (7)

<220>  
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aggaagacat	atggaaggct	acctataaat	gtntaggnt	cantncgatg	ggagggnctt	120
tttagcatcg	ttcttgtgcc	cttgacctct	cttgttaagt	atggatcgca	ggaagtcaa	180
ctcatgactt	ttggacagcc	tcgggtaggc	aatccttctt	ttgctgcgta	cttcagtgc	240
caagtcgccg	gaacaatccg	tgtgacccat	cagaatgaca	ttgtcccaca	cttgccacca	300
tatttttgtc	accttggcga	atggacatat	caccacttct	cgagagaggt	ttggcttcat	360
gagaccatag	taggaaatgt	agttactagg	aatgagacca	tctgtgatgg	atcaggcgag	420
gacccaacat	gc					432

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<210> 28
<211> 106
<212> PRT
<213> Oryza sativa
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<400> 28  
Gly Pro Phe Ser Ile Val Leu Val Pro Leu Thr Ser Leu Val Lys Tyr  
1 5 10 15

Gly Ser Gln Glu Val Gln Leu Met Thr Phe Gly Gln Pro Arg Val Gly  
20 25 30

Asn Pro Ser Phe Ala Ala Tyr Phe Ser Asp Gln Val Pro Arg Thr Ile  
35 40 45

Arg Val Thr His Gln Asn Asp Ile Val Pro His Leu Pro Pro Tyr Phe  
50 55 60

Cys Tyr Leu Gly Glu Trp Thr Tyr His His Phe Ser Arg Glu Val Trp  
65 70 75 80

Leu His Glu Thr Ile Val Gly Asn Val Val Thr Arg Asn Glu Thr Ile  
85 90 95

Cys Asp Gly Ser Gly Glu Asp Pro Thr Cys  
100 105

<210> 29  
 <211> 1234  
 <212> DNA  
 <213> Glycine max

<400> 29  
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 ccacaaccca agtcttgatt gttttggaca agcatgagaa ccgcgatact tatgtggtag 120  
 ctttccgagg aacggaaccc tttgatgcag atgcatgggt cactgacctt gacatctcat 180  
 ggtacgcatt cccggcattg gaaaaatgca tgggtggcttc atgaaagcct tagggctaca 240  
 gaaaaatgtg ggggtggccta aggagattca aagggatgaa aatcttcccc cgttggccta 300  
 ctatgttatt agggacattc taaggaaagg tttgagtga aatcctaattg caaagtttat 360  
 cattacgggt catagttttg gtggagcact cgcaatcttg taccctacga tcatgttctt 420  
 gcatgatgag aagttgctga ttgagagggt ggaagggatc tacacgtttg ggcaaccaag 480  
 agttggagat gaagcatatg cacagtatat gagacaaaaa ttgagggaaa attctatcag 540  
 gtattgcagg tttgtttatt gcaatgacat agttccgagg ttgccctatg atgataagga 600  
 cttgctcttc aagcactttg ggatctgcct tttctttaac aggcgctatg aactcaggat 660  
 tctcgaagaa gagccgaata agaactattt ctgcgccatg tgtgtgatac ccatgatgtt 720  
 caatgctgtt ttggaactaa taaggagctt taccatagcg tacaaaaatg gaccticata 780  
 tagagaagga tggtttctct ttagtttcag gttggttgg ctgctgattc ctggcttacc 840  
 tgctcacggg ccacaagatt atattaattc cactcttctg ggatcaattg aaaaacattt 900  
 taaagcagat tgatgtgtcc gtatacatga tcattccata ccactacgta catgtgtatg 960  
 gtcatgcaga ctaaaattta cataatcaag atttttagtt ttagaaaaaa tggtaataac 1020  
 acttgattat gtatcatgtg aagaatagtt atgtatcata atgatcatga ataataaac 1080  
 agtttgctcg cagtacgagt tattgtatag taattaataa gctagggtta aagttgtttc 1140  
 ctttggtgca tggatttatc attaattgaga tcaatgtgaa gtttgtttat ttcaaaaaaa 1200  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1234

<210> 30  
 <211> 246  
 <212> PRT  
 <213> Glycine max

<400> 30  
 His Leu Met Val Arg Ile Pro Gly Ile Gly Lys Met His Gly Gly Phe  
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 Met Lys Ala Leu Gly Leu Gln Lys Asn Val Gly Trp Pro Lys Glu Ile  
 20 25 30  
 Gln Arg Asp Glu Asn Leu Pro Pro Leu Ala Tyr Tyr Val Ile Arg Asp  
 35 40 45  
 Ile Leu Arg Lys Gly Leu Ser Glu Asn Pro Asn Ala Lys Phe Ile Ile  
 50 55 60  
 Thr Gly His Ser Leu Gly Gly Ala Leu Ala Ile Leu Tyr Pro Thr Ile  
 65 70 75 80  
 Met Phe Leu His Asp Glu Lys Leu Leu Ile Glu Arg Leu Glu Gly Ile  
 85 90 95  
 Tyr Thr Phe Gly Gln Pro Arg Val Gly Asp Glu Ala Tyr Ala Gln Tyr  
 100 105 110  
 Met Arg Gln Lys Leu Arg Glu Asn Ser Ile Arg Tyr Cys Arg Phe Val  
 115 120 125  
 Tyr Cys Asn Asp Ile Val Pro Arg Leu Pro Tyr Asp Asp Lys Asp Leu  
 130 135 140

Leu Phe Lys His Phe Gly Ile Cys Leu Phe Phe Asn Arg Arg Tyr Glu  
 145 150 155 160

Leu Arg Ile Leu Glu Glu Glu Pro Asn Lys Asn Tyr Phe Ser Pro Trp  
 165 170 175

Cys Val Ile Pro Met Met Phe Asn Ala Val Leu Glu Leu Ile Arg Ser  
 180 185 190

Phe Thr Ile Ala Tyr Lys Asn Gly Pro His Tyr Arg Glu Gly Trp Phe  
 195 200 205

Leu Phe Ser Phe Arg Leu Val Gly Leu Leu Ile Pro Gly Leu Pro Ala  
 210 215 220

His Gly Pro Gln Asp Tyr Ile Asn Ser Thr Leu Leu Gly Ser Ile Glu  
 225 230 235 240

Lys His Phe Lys Ala Asp  
 245

<210> 31  
 <211> 490  
 <212> DNA  
 <213> Glycine max

<400> 31  
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 tacgggtcat agtcttggtg gagcacttgc aattcttttt cccgctatgc taattttgca 180  
 tgctgagaca tttcttttgg aaaggcttga aggggtgtac acatttggac agcctagggt 240  
 tggagatgaa acatttgcta aatacatgga aaatcaattg aaacattatg gcattaagta 300  
 ttttaggttt gtttactgca acgatattgt tcctagggtg ccctttgatg aagatatcat 360  
 gaaatttgag cattttggga catgtcttta ttatgacagg agctatacat gcaagggtaca 420  
 tatataagta ttttaatttt ttgattcatg catatatctg tcattgtaat caactttttt 480  
 ttttctgggg 490

<210> 32  
 <211> 141  
 <212> PRT  
 <213> Glycine max

<400> 32  
 His Glu Glu Arg Trp Pro Lys Glu Ile Glu Thr Asp Glu Asn Arg Pro  
 1 5 10 15

Arg Val Tyr Tyr Ser Ile Arg Asp Leu Leu Lys Lys Cys Leu Asn Arg  
 20 25 30

Asn Asp Lys Ala Lys Phe Ile Leu Thr Gly His Ser Leu Gly Gly Ala  
 35 40 45

Leu Ala Ile Leu Phe Pro Ala Met Leu Ile Leu His Ala Glu Thr Phe  
 50 55 60

Leu Leu Glu Arg Leu Glu Gly Val Tyr Thr Phe Gly Gln Pro Arg Val  
 65 70 75 80

Gly Asp Glu Thr Phe Ala Lys Tyr Met Glu Asn Gln Leu Lys His Tyr  
 85 90 95



Gly	Ile	Lys	Tyr	Phe	Arg	Phe	Val	Tyr	Cys	Asn	Asp	Ile	Val	Pro	Arg
			100					105					110		
Leu	Pro	Phe	Asp	Glu	Asp	Ile	Met	Lys	Phe	Glu	His	Phe	Gly	Thr	Cys
		115					120					125			
Leu	Tyr	Tyr	Asp	Arg	Ser	Tyr	Thr	Cys	Lys	Val	His	Ile			
	130					135					140				

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<210> 33
<211> 774
<212> DNA
<213> Triticum aestivum
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<212> PRT  
 <213> Canis familiaris

<400> 35

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Thr	His	Gly	Leu	Phe	Gly	Lys	Leu	His	Pro	Thr	Asn	Pro	Glu	Val	Thr	20	25	30	
Met	Asn	Ile	Ser	Gln	Met	Ile	Thr	Tyr	Trp	Gly	Tyr	Pro	Ala	Glu	Glu	35	40	45	
Tyr	Glu	Val	Val	Thr	Glu	Asp	Gly	Tyr	Ile	Leu	Gly	Ile	Asp	Arg	Ile	50	55	60	
Pro	Tyr	Gly	Arg	Lys	Asn	Ser	Glu	Asn	Ile	Gly	Arg	Arg	Pro	Val	Ala	65	70	75	80
Phe	Leu	Gln	His	Gly	Leu	Leu	Ala	Ser	Ala	Thr	Asn	Trp	Ile	Ser	Asn	85	90	95	
Leu	Pro	Asn	Asn	Ser	Leu	Ala	Phe	Ile	Leu	Ala	Asp	Ala	Gly	Tyr	Asp	100	105	110	
Val	Trp	Leu	Gly	Asn	Ser	Arg	Gly	Asn	Thr	Trp	Ala	Arg	Arg	Asn	Leu	115	120	125	
Tyr	Tyr	Ser	Pro	Asp	Ser	Val	Glu	Phe	Trp	Ala	Phe	Ser	Phe	Asp	Glu	130	135	140	
Met	Ala	Lys	Tyr	Asp	Leu	Pro	Ala	Thr	Ile	Asp	Phe	Ile	Leu	Lys	Lys	145	150	155	160
Thr	Gly	Gln	Asp	Lys	Leu	His	Tyr	Val	Gly	His	Ser	Gln	Gly	Thr	Thr	165	170	175	
Ile	Gly	Phe	Ile	Ala	Phe	Ser	Thr	Asn	Pro	Lys	Leu	Ala	Lys	Arg	Ile	180	185	190	
Lys	Thr	Phe	Tyr	Ala	Leu	Ala	Pro	Val	Ala	Thr	Val	Lys	Tyr	Thr	Glu	195	200	205	
Thr	Leu	Leu	Asn	Lys	Leu	Met	Leu	Val	Pro	Ser	Phe	Leu	Phe	Lys	Leu	210	215	220	
Ile	Phe	Gly	Asn	Lys	Ile	Phe	Tyr	Pro	His	His	Phe	Phe	Asp	Gln	Phe	225	230	235	240
Leu	Ala	Thr	Glu	Val	Cys	Ser	Arg	Glu	Thr	Val	Asp	Leu	Leu	Cys	Ser	245	250	255	
Asn	Ala	Leu	Phe	Ile	Ile	Cys	Gly	Phe	Asp	Thr	Met	Asn	Leu	Asn	Met	260	265	270	
Ser	Arg	Leu	Asp	Val	Tyr	Leu	Ser	His	Asn	Pro	Ala	Gly	Thr	Ser	Val	275	280	285	
Gln	Asn	Val	Leu	His	Trp	Ser	Gln	Ala	Val	Lys	Ser	Gly	Lys	Phe	Gln	290	295	300	



